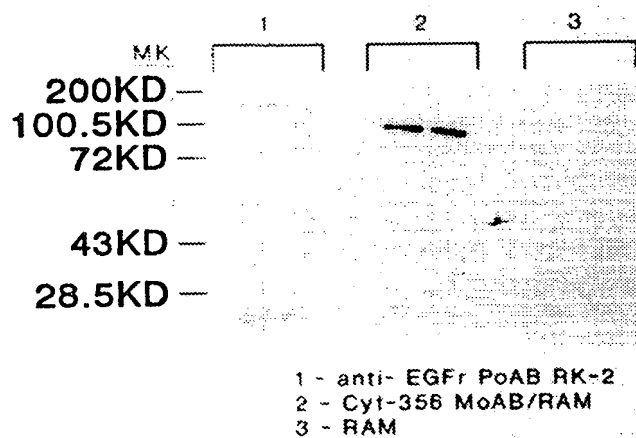


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FIGURE 1

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FIGURE 2A

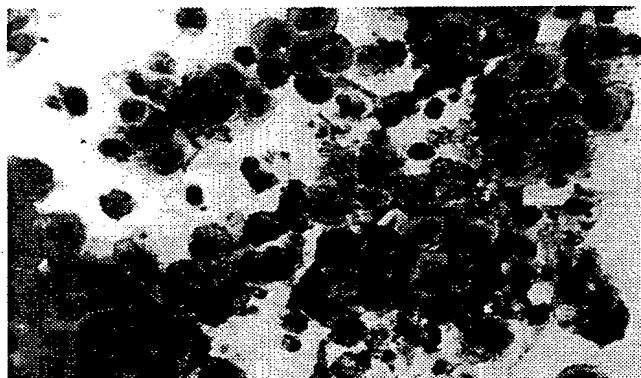


FIGURE 2B

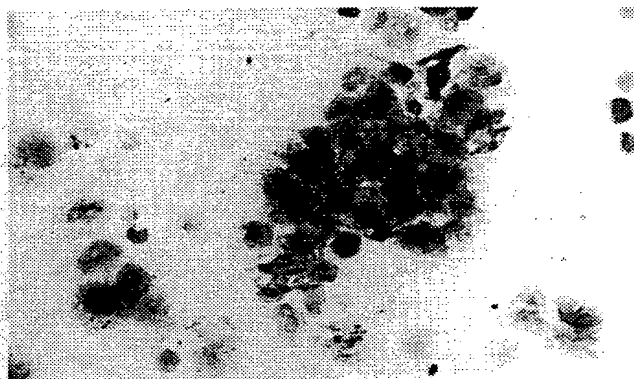


FIGURE 2C

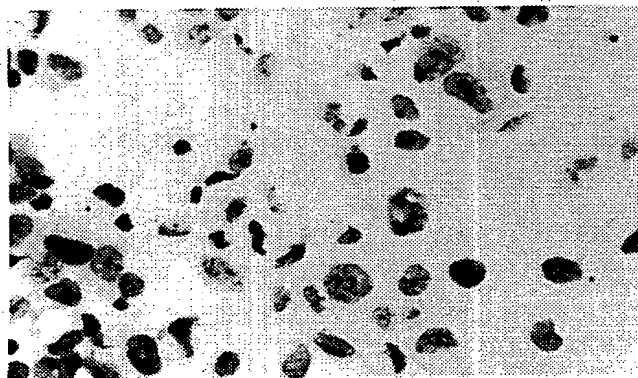
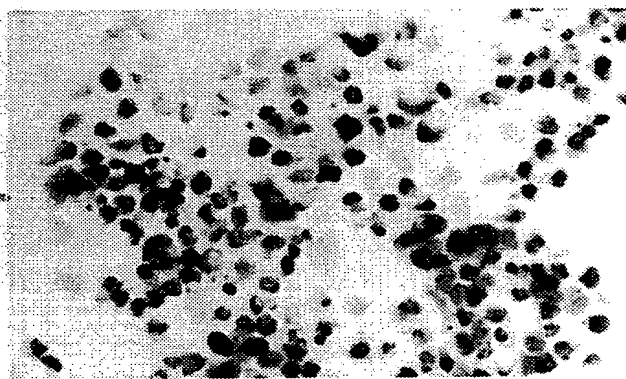


FIGURE 2D



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FIGURE 3A

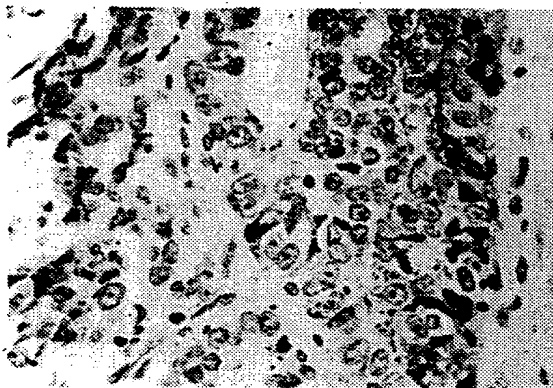


FIGURE 3B

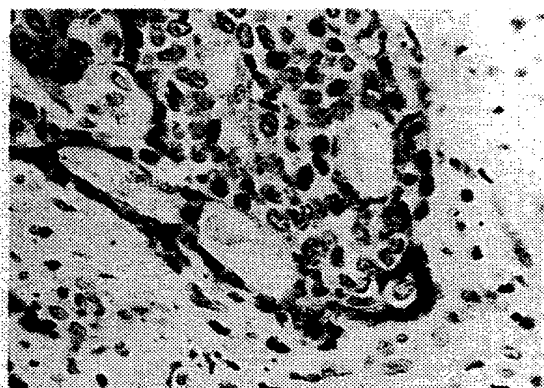


FIGURE 3C

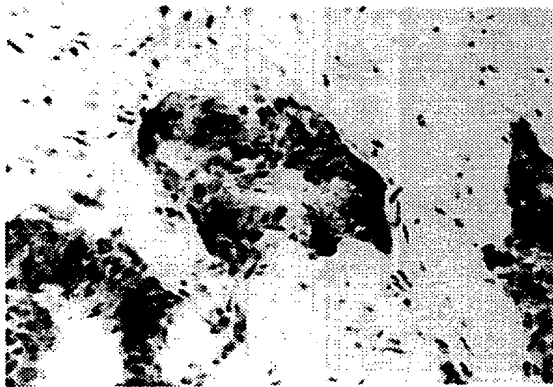
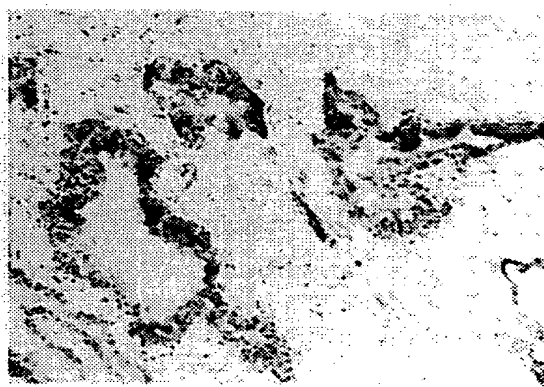


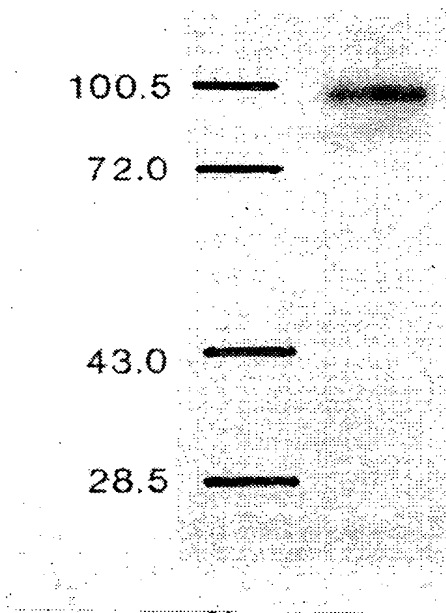
FIGURE 3D



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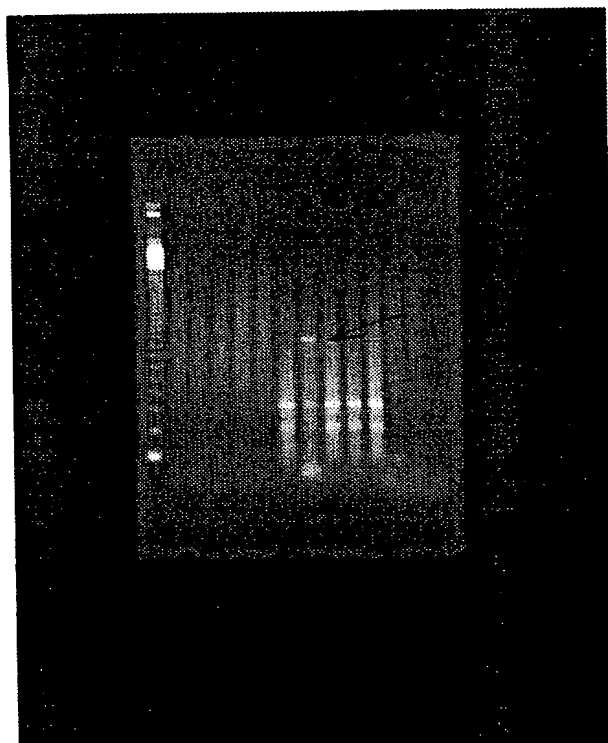
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FIGURE 4



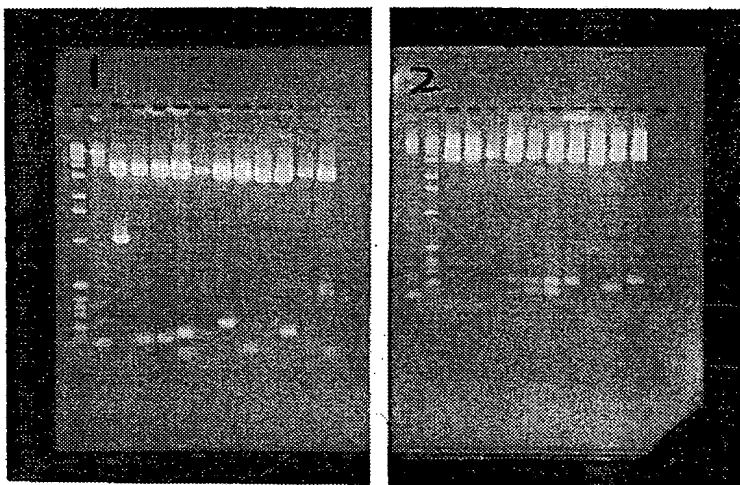
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FIGURE 5



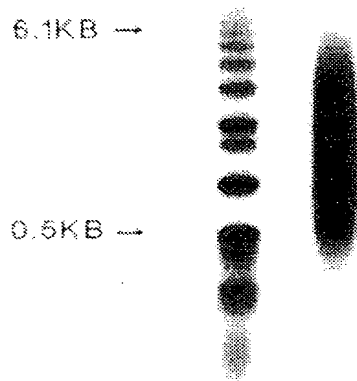
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FIGURE 6A **FIGURE 6B**



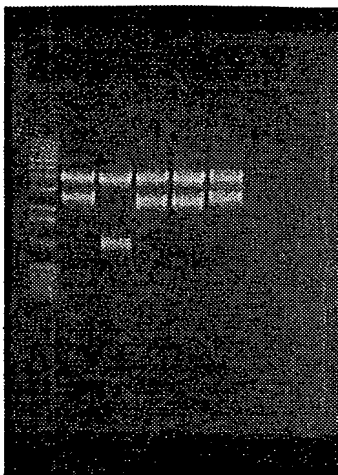
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FIGURE 7



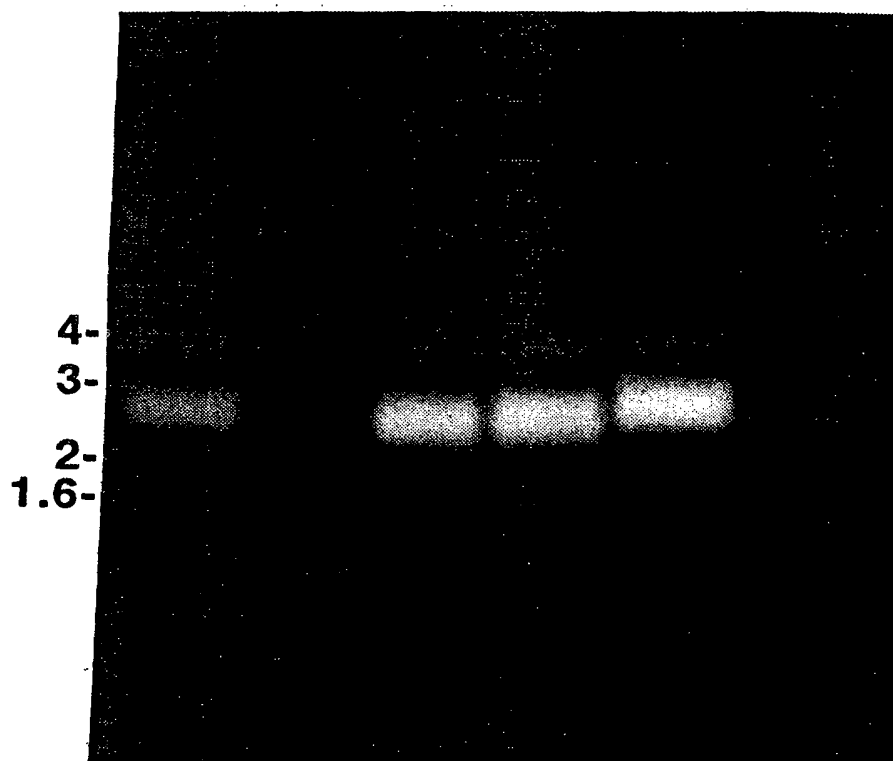
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FIGURE 8



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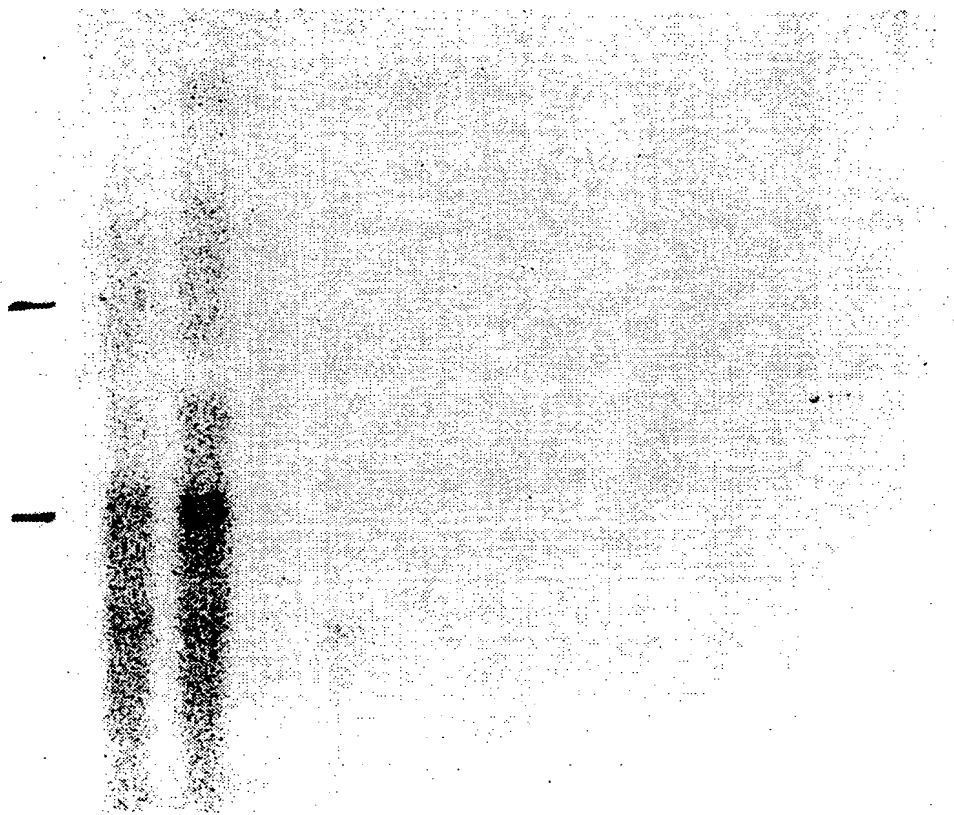
FIGURE 9



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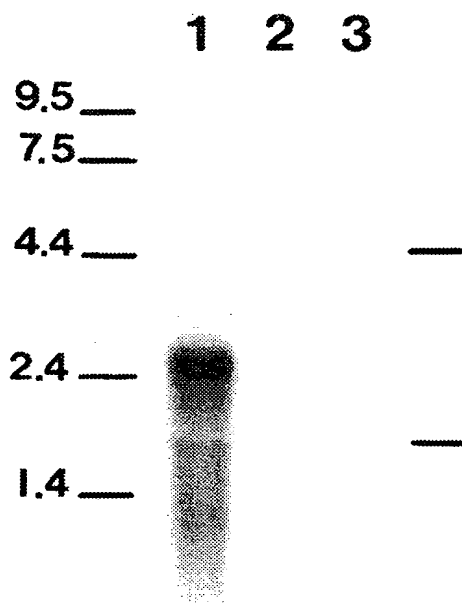
FIGURE 10



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FIGURE 11



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FIGURE 12A

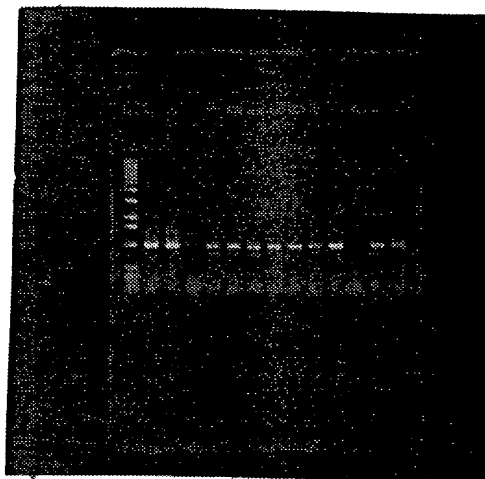
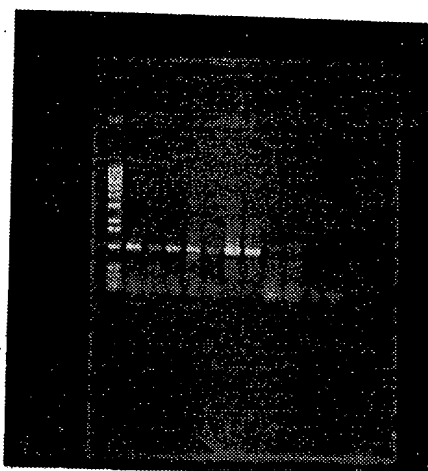


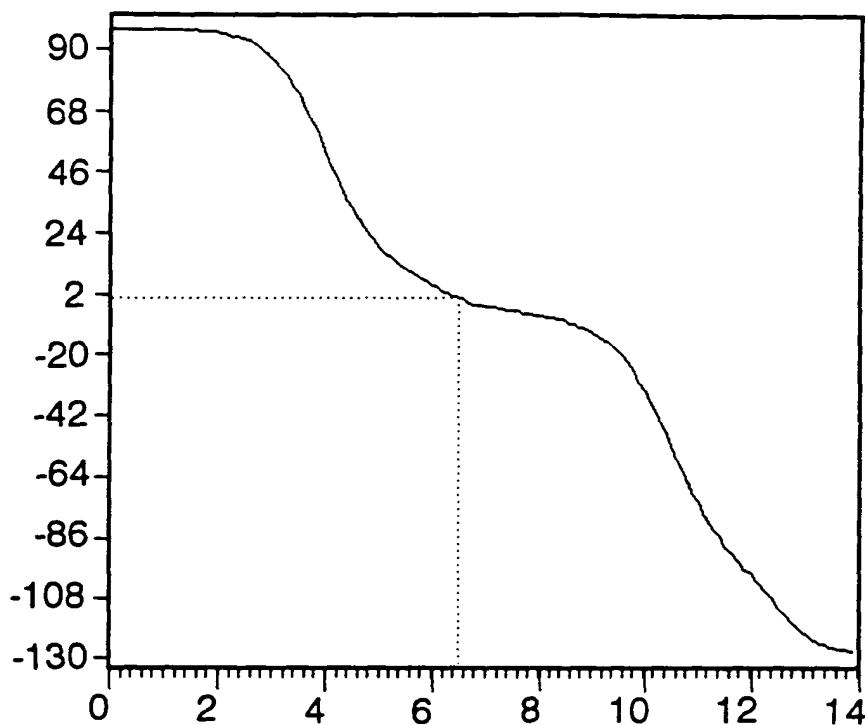
FIGURE 12B



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FIGURE 13



Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

In Helical	(H)	conformation	[DC =	-75	CNAT] :	264	AA =>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT] :	309	AA =>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT] :	76	AA =>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT] :	101	AA =>	13.4%

Sequence shown with conformation codes.

Consecutive stretch of 5 or more residues in a given conformation are overlined.

[illegible]

FIGURE 14-3

[illegible]

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FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X Extended conformation: -
 Turn conformation: > Coil conformation: *

10	20	30	40	50
MWNLLHETDS	AVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT			
XXXXXXXXXXXX	-----XXXXXXXXXXXX			
XXXXXXXXXXXX	-----XXXXXXXXXXXX			
60	70	80	90	100
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQN	FQLAKQIQSQW			

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FIGURE 14-5

```

XXXXXXXXXXXXXXXXXXXX-->>>-----XXXXXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXXXX-->>>-----XXXXXXXXXXXXX-X*--

      110      120      130      140      150
      |        |        |        |        |
KEFGLDSVELAHYDVLLSYPNKTHPNYISIIINEDGNEIFNTSLFEPPPG

->>***XXXXXXXXXX-->>>***----->***>>>***>>
->>***XXXXXXXXXX-->>>***----->***>>>***>>

      160      170      180      190      200
      |        |        |        |        |
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI

```

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FIGURE 14-6

```

>----->--**>-----XXXXXXXXXXXXXXXXXX>>--
>----->--**>-----XXXXXXXXXXXXXXXXXX>>--

210      220      230      240      250
|         |         |         |
VIARYGVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG

----->>**XXXXXXXX----->>----->>>>--**>
----->>**XXXXXXXX----->>----->>>>--**>

260      270      280      290      300
|         |         |         |
GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY

>*----->>*-----**-----XX-----**-----
>*----->>*-----**-----XX-----**-----

310      320      330      340      350
|         |         |         |
DAQKLEKMGSAAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTN

XXXXXXXX-->>***>-->>-->-----*--*XXXXXX--*--*--*
XXXXXXXX-->>***>-->>-->-----*--*XXXXXX--*--*--*

360      370      380      390      400
|         |         |         |
EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR

```


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FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXXXXXX-X-----XXXXX----->XXX
 -----XXXXXXXXXXXXXXXXX-X-----XXXXX----->XXX

610 620 630 640 650
 | | | | |
 AVVLRKYADKIYISMKHPQEMKTYSVSFDLSFSAVKNFTEIASKFSERL

XXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
 XXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX

660 670 680 690 700
 | | | | |
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHHVIYAPSSHNY

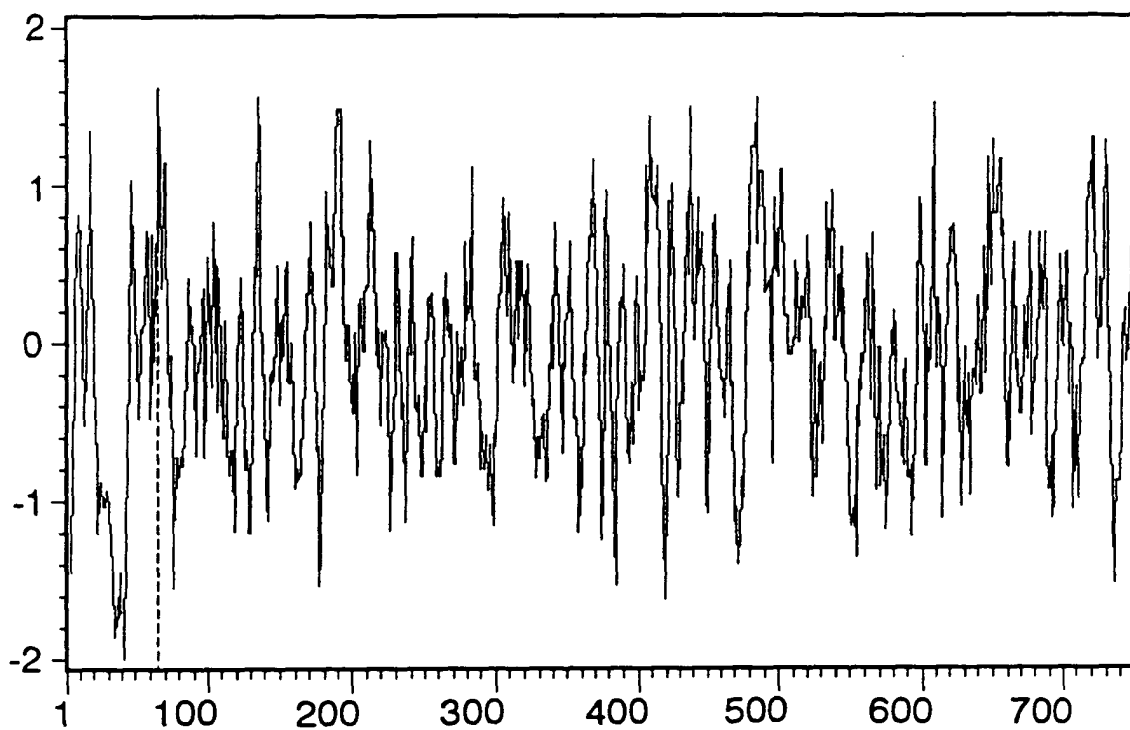
XX>>>*>-----XXXXXXXXXX-->>***>----->***>
 XX>>>*>-----XXXXXXXXXX-->>***>----->***>

710 720 730 740 750
 | | | | |
 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAETLSEVA

----->-----XXXXXXXXXX*XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX
 ----->-----XXXXXXXXXX*XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX

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FIGURE 15A



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FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1)	Ah= 1.62	: From	63 to	68	: Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah= 1.57	: From	132 to	137	: Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah= 1.55	: From	482 to	487	: Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point: gave a proportion of 33% of incorrect predictions.

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FIGURE 16-1

The best scores are:

		initn	init1	opt
CHKTFER	G.gallus mRNA for transferrin receptor	203	120	321
RATTRFR	Rat transferrin receptor mRNA, 3' end.	164	164	311
HUMTFRR	Human transferrin receptor mRNA, complete cd	145	145	266

CHKTFER G.gallus mRNA for transferrin receptor 203 120 321
51.9% identity in 717 nt overlap

1020 1030 1040 1050 1060 1070
pmsgen TGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA

CHKTFE TACACTTATCCCATTCGGACATGCCACCTTGGAACTGGAGACCCCTTACACCCAGGCTT
990 1000 1010 1020 1030 1040

1080 1090 1100 1110 1120 1130
pmsgen CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT

CHKTFE CCCTTCGTTCAACCCACACCCA---GTTCCACCAGTTGAATCTTCAGGACTACCCACAT
1050 1060 1070 1080 1090 1100

1140 1150 1160 1170 1180 1190
pmsgen TCCTGTTCAATCCAAATGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC

CHKTFE TGCTGTTCAGACCATCTCTAGCAGTGCAGCAGCCAGGCTGTTTCAGCAAAATGGATGGAGA
1110 1120 1130 1140 1150 1160

FIGURE 16-7

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1550	1560	1570	1580	1590	1600
pmsgen	CTTGGTTCTACTGAGTGGGCAGAGGAGAA---	TTCAAGACTCCTTCAAGAGCGTGGCGTG			
	::::: : ::::: : : : : X ::::: : : : : : : : : :				
RATTRF	GTTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTTCATCTTTGCATCTAAAG---	GCTTTC			
970	980	990	1000	1010	1020
1610	1620	1630	1640	1650	1660
pmsgen	GCTTATATTAATGCTGACTCATCTATAGAAAGAACTA-C	ACTCTGAGAGTTGATGTAC			
	::::: : ::::: : : : : : : : : : : : : : : : : : :				
RATTRF	ACTTACATTAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG				
1030	1040	1050	1060	1070	1080
1670	1680	1690	1700	1710	1720
pmsgen	ACCGCTGATGTACAGCTTGGTACACAACTTAACAAAGAGCTGAAAGC-CCTGATGAAG				
	::: :				
RATTRF	CCCCCTATTATATACACTTATGGGGAAGATAATGCAGGA--CGTAAAGCATCCGA-----				
1090	1100	1110	1120	1130	

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FIGURE 16-8

```

1730      1740      1750      1760      1770
pmsgen  GCTTTGAAGGCAAAATCTCTTTAT-GAA-----AGTTGGACTAAATAAGTCCCTTCCCCCAG
          :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RATTRF  ---TTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
1140      1150      1160      1170      1180      1190

1780      1790      1800      1810      1820      1830
pmsgen  AGTCAGTGGCATGCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTCTCT
          CCTTGGACAAATGCTGCATTCCCTTTTCTTGCCATATTCAGGAAATCCCAGCAGTTTCTTCTCT
1200      1210      1220      1230      1240      1250

```

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```

1400      1410      1420      1430      1440      1450
pmsgen CCGGACTCATGGGTGTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTGTTTCATG
      : : : : : : : : : : : : : : : : : :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
1320      1330      1340      1350      1360      1370

```

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FIGURE 16-10

```
1460      1470      1480      1490      1500
pmsgen AAATTG---TGAGGAGCTTTGGAACACTGAAAGGAAGGTGGAGACCTAGAAACAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR AACTTGCCAGATGTTCTCAGATATGGTCTTAAAGATGGGTTTCAGCCCAGCAGAAGCA
1380      1390      1400      1410      1420      1430

1510      1520      1530      1540      1550      1560
pmsgen TTTTGTTGCAAGCTGGGATGCAGAAGAAATTGGTCTTCTTGGTTCTACTGAGTGGGCAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR TTATCTTTGCCAGTTGGAGTGCTGGAGACTTTGGATCGGTGGTGCCACTGAATGGCTAG
1440      1450      1460      1470      1480      1490

1570      1580      1590      1600      1610      1620
pmsgen A-GGAGAAATTCAGACTCCTTCAAGAGCGTGGCGTTGCTTATATTAATGCTGACTCATCT
      : :: : : : :: :: : : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR AGGATACCTTTCGTC-CCTGCATTAAAGGCTTTCACCTTATATTAATCTGGATAAAGCG
1500      1510      1520      1530      1540      1550

1630      1640      1650      1660      1670      1680
pmsgen ATAGAAGAAACTACACTCTGAGAGTTGATGTACACCGCTGATGTACA-GCTTGGT-AC
      : :: : : : :: : : : : : : : : : : : : : : : : : : : : : : : :
HUMTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACCTGTTGTATACGCTTATTGAG
1560      1570      1580      1590      1600      1610
```

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FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTATG				
:	:	:	:	:	:
:	:	:	:	:	:
HUMTFR	AAAACAATGCACAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

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FIGURE 17A

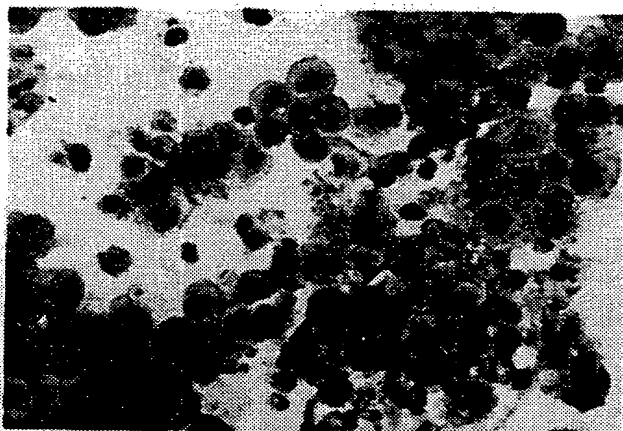


FIGURE 17B

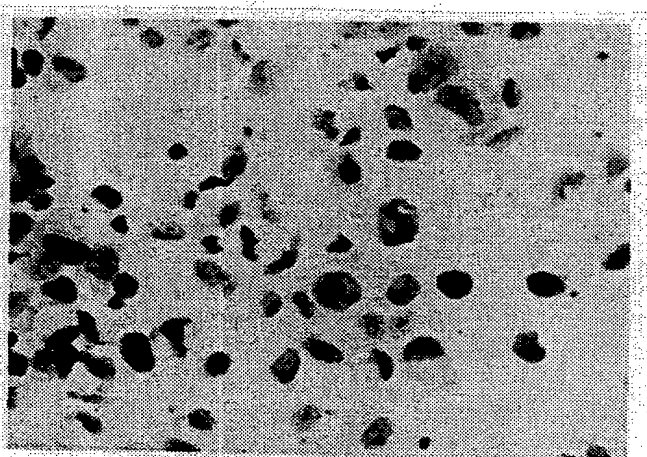
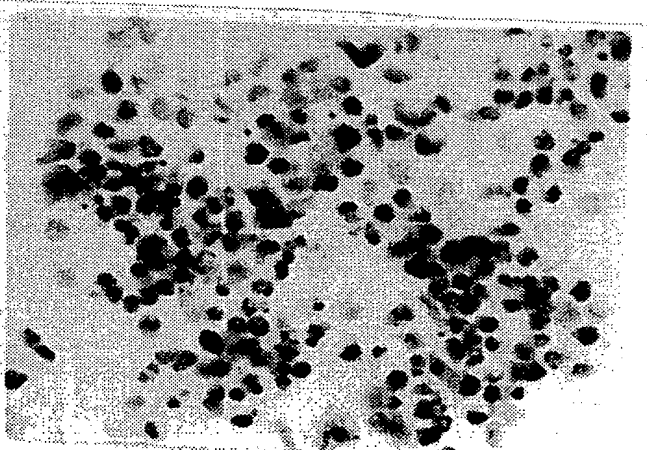
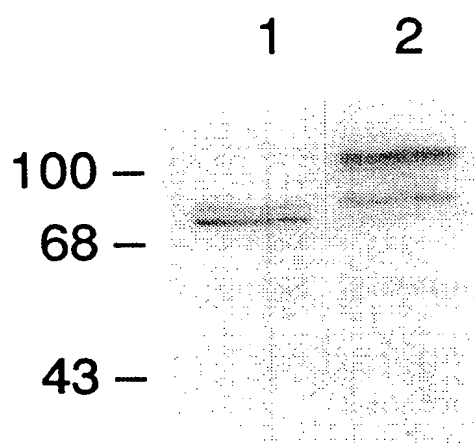


FIGURE 17C



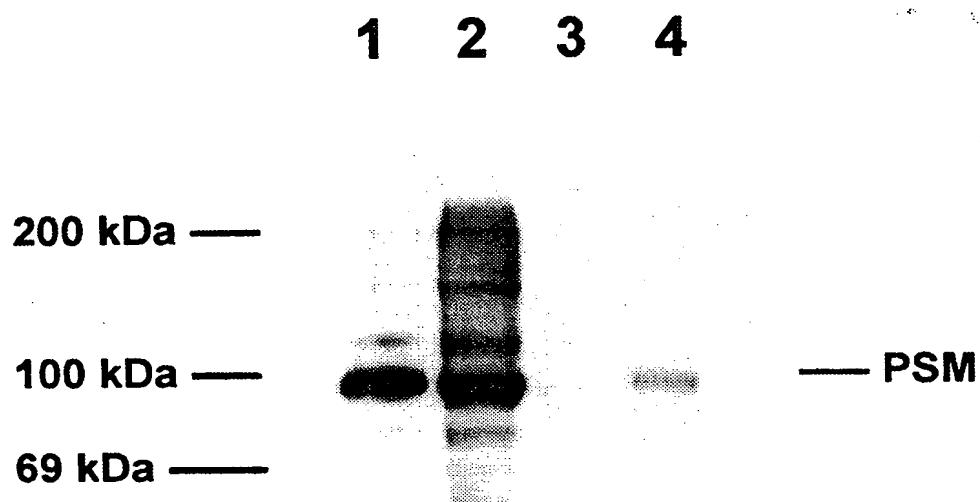
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FIGURE 18



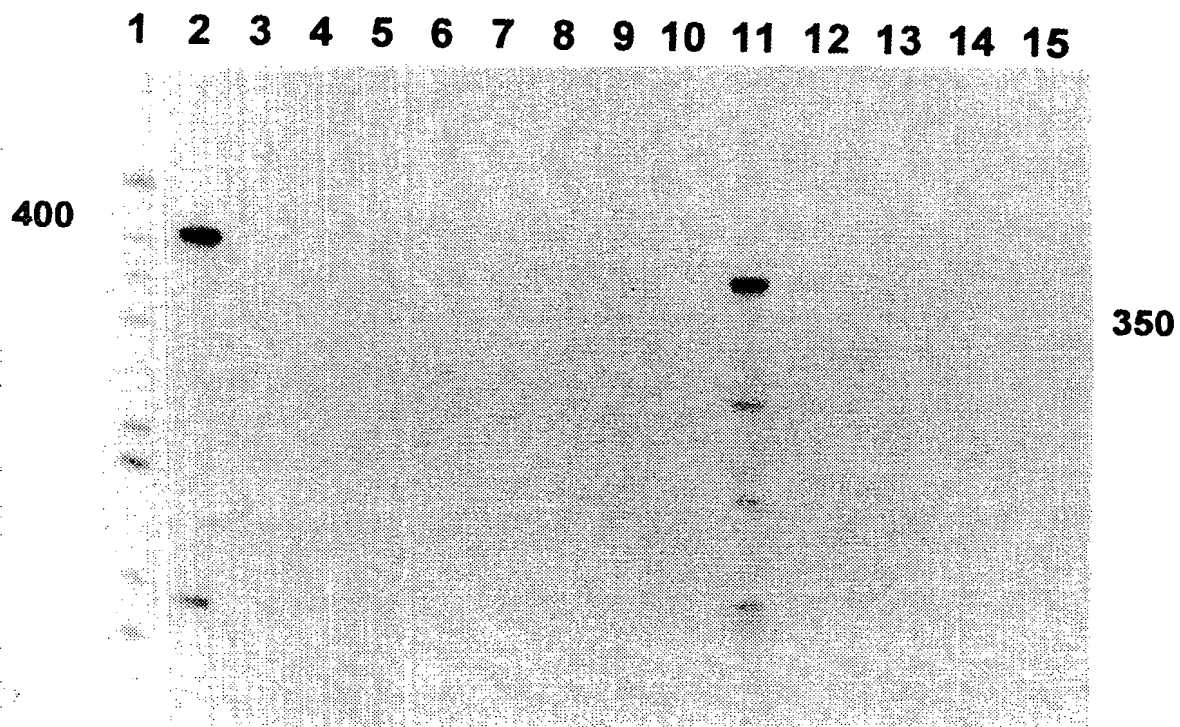
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FIGURE 19



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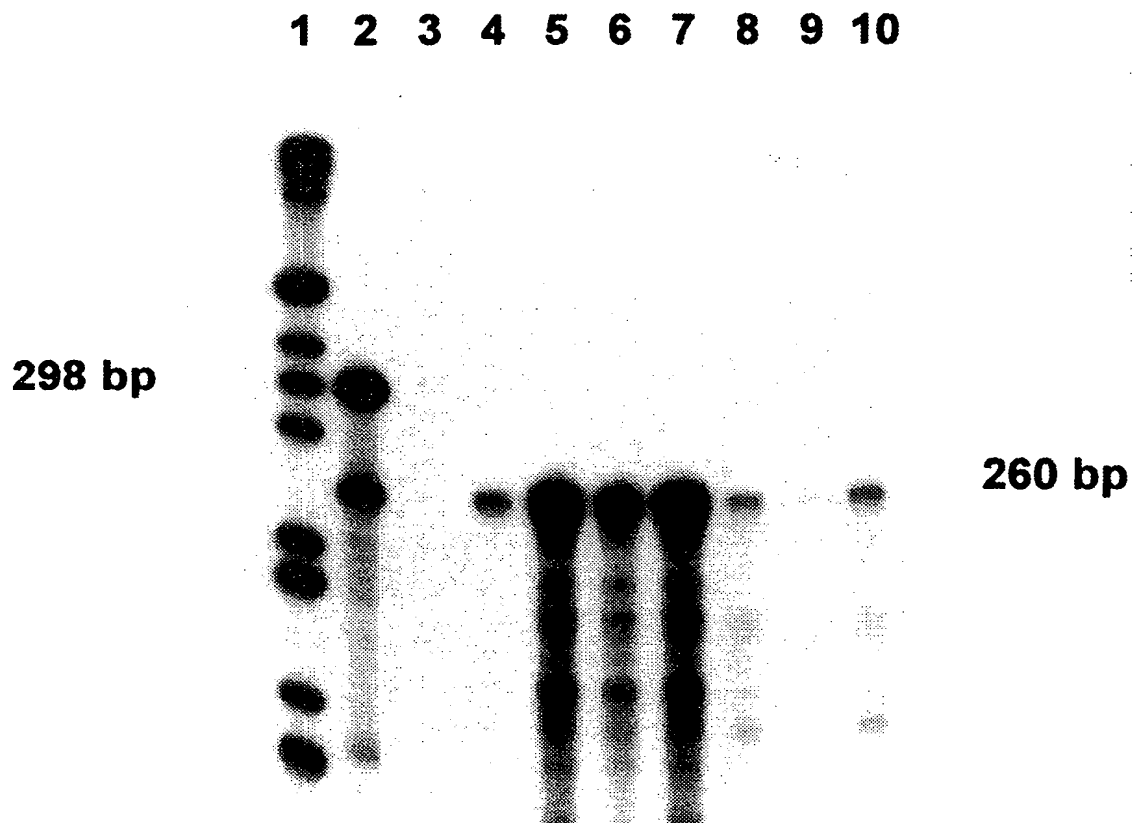
FIGURE 20





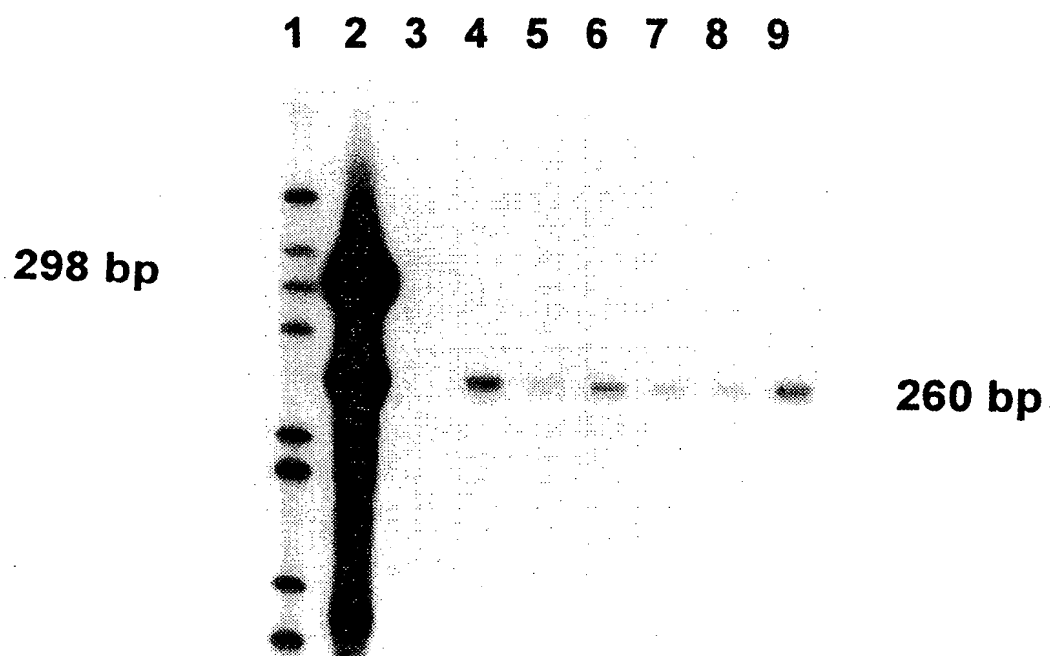
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FIGURE 21



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FIGURE 22



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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

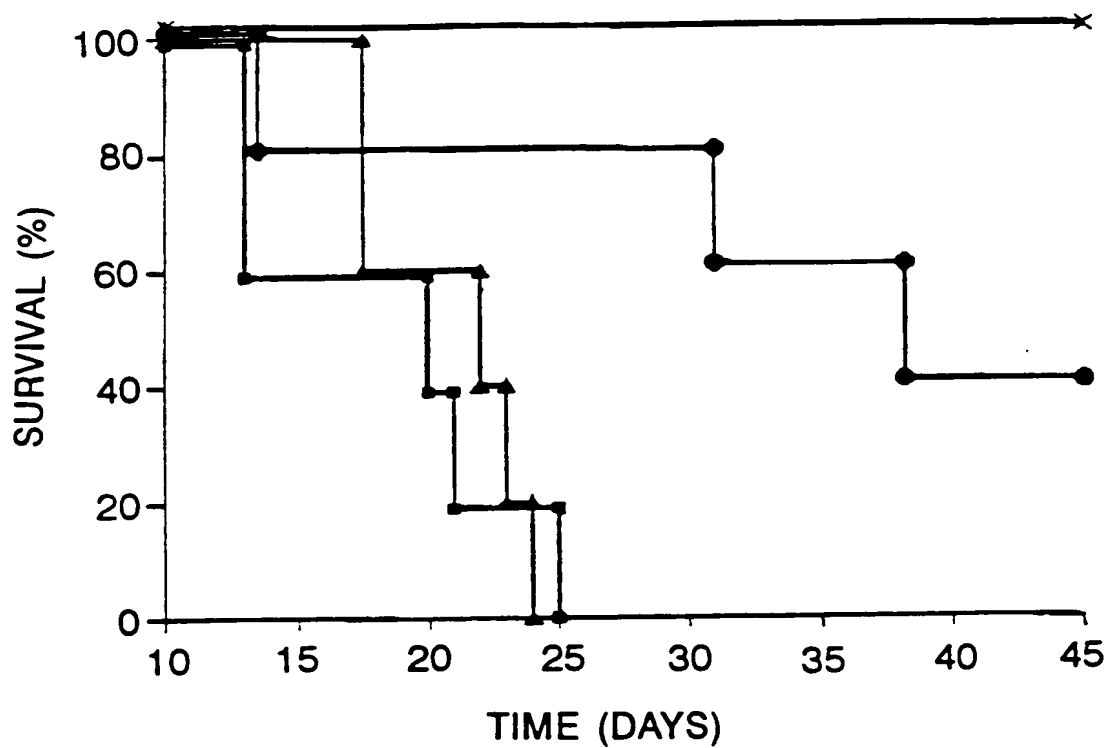
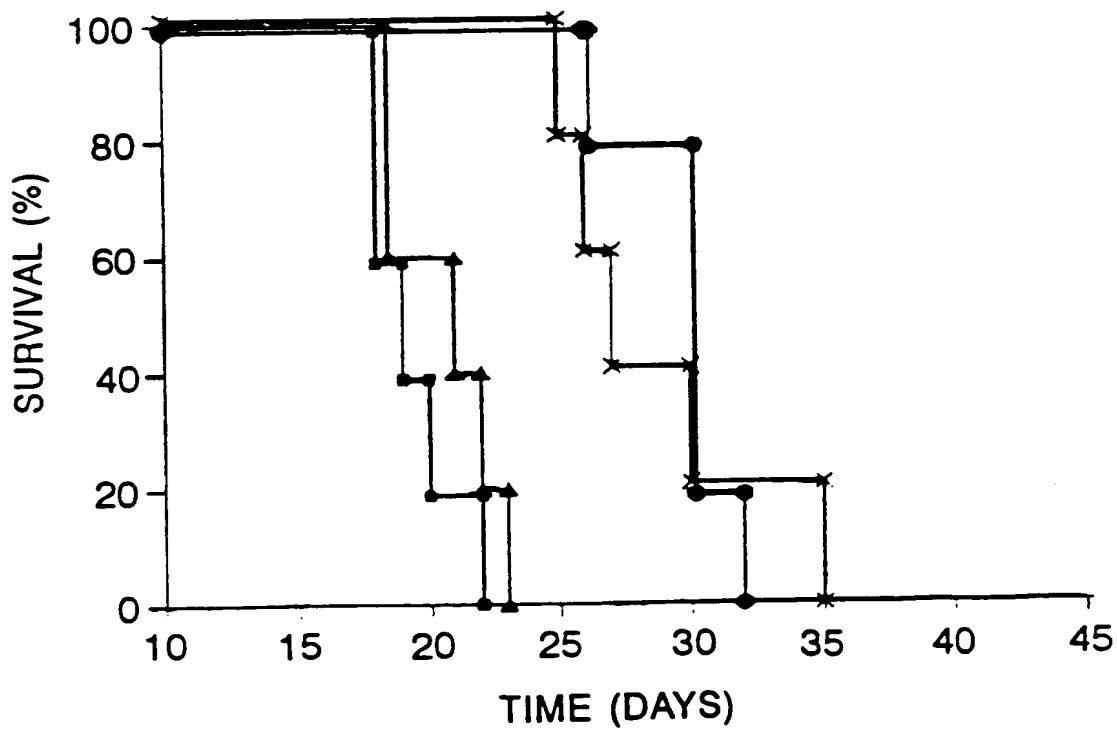


FIGURE 24B



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FIGURE 25A

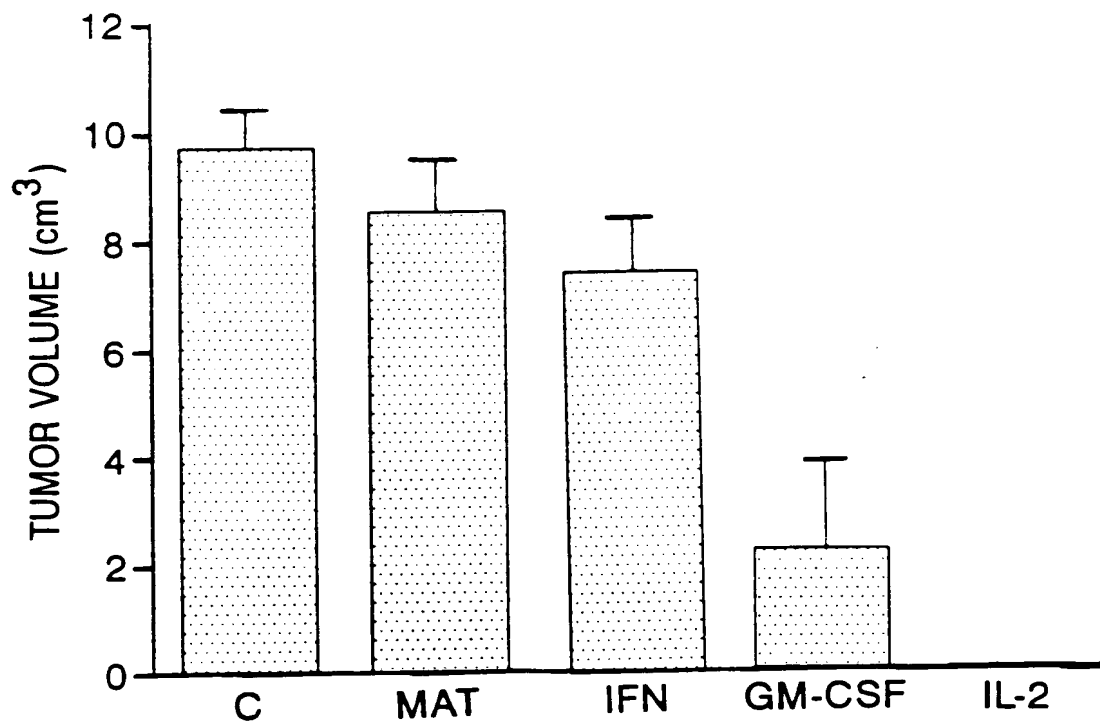
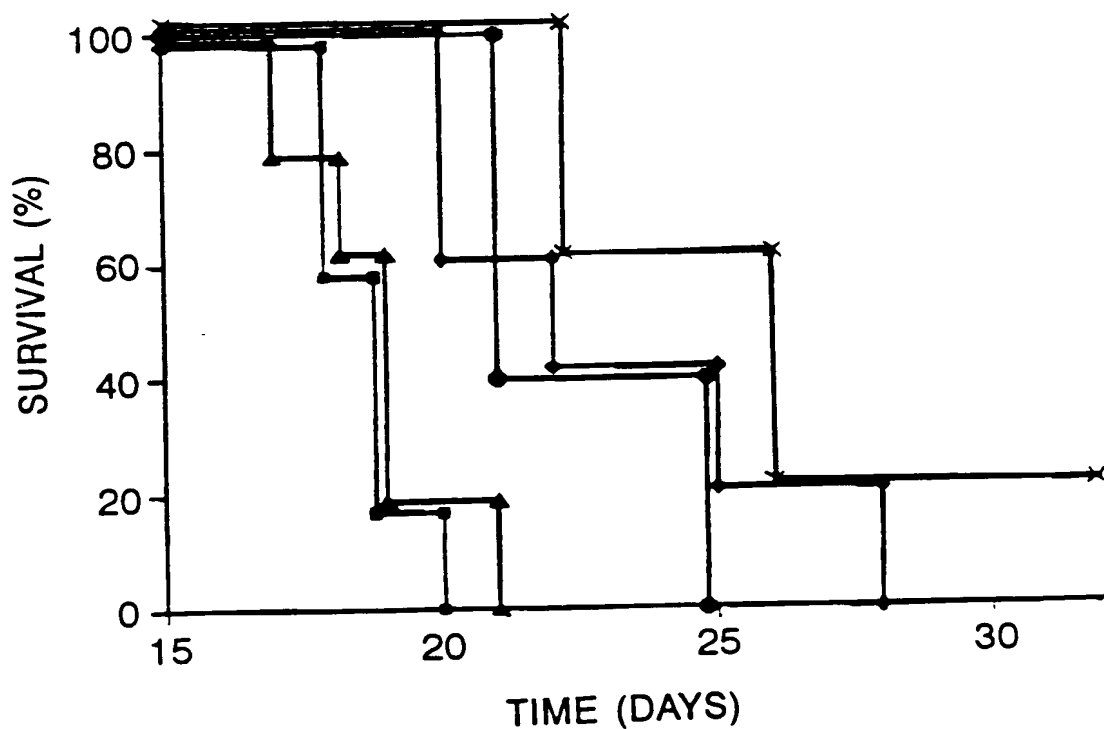
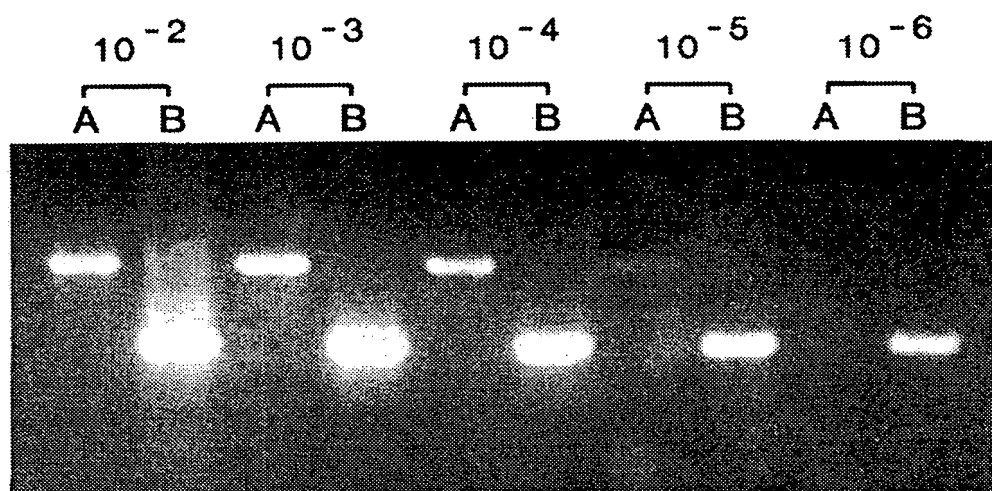


FIGURE 25B



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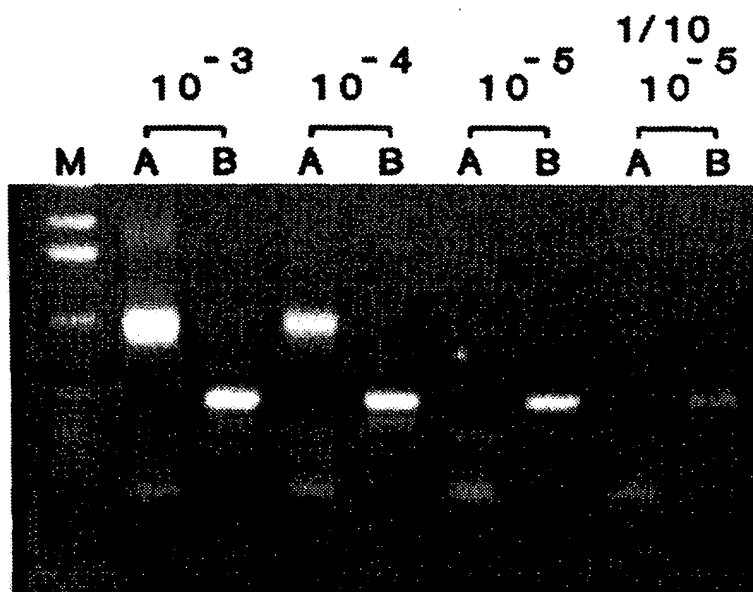
FIGURE 26



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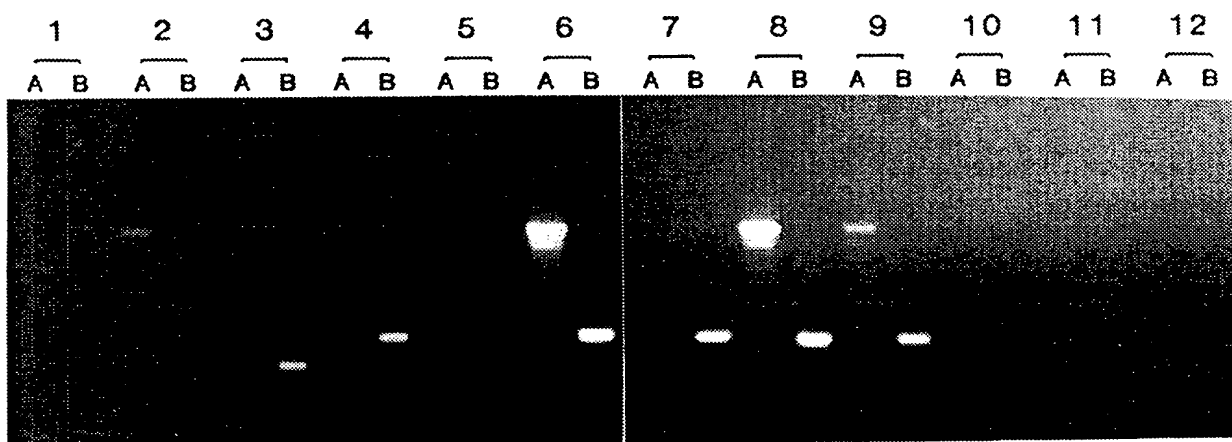
FIGURE 27



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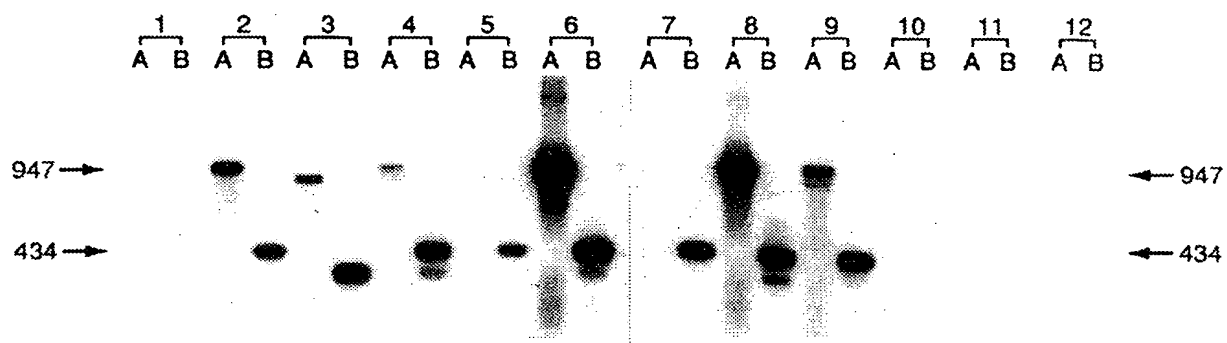
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-